

SEQUENCE LISTING

(1)

GENERAL INFORMATION

(i) APPLICANT: NOBUTO YAMAMOTO

(ii) TITLE OF INVENTION: PREPARATION OF POTENT
MACROPHAGE ACTIVATING FACTORS
DERIVED FROM CLONED VITAMIN D
BINDING PROTEIN AND ITS DOMAIN
AND THEIR THERAPEUTIC USAGE
FOR CANCER, HIV-INFECTION AND
OSTEOPETROSIS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CAESAR, RIVISE, BERNSTEIN,
COHEN & POKOTILOW, LTD.

(B) STREET: 1635 Market Street, 12th Floor

(C) CITY: Philadelphia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19103-2212

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb

(B) COMPUTER: IBM PC Compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WORDPERFECT VERSION 4.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: March 19, 1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/478,121

(B) FILING DATE: 07-JUNE-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Robert S. Silver

(B) REGISTRATION NO.: 35,681

(C) REFERENCE/DOCKET NUMBER:Y1004/20002

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 567-2010

(B) TELEFAX: (215) 751-1142

(2) INFORMATION FOR SEQ ID NO: 1:

[i] SEQUENCE CHARACTERISTICS:

[A] LENGTH: 458 amino acids

[B] TYPE: amino acid

[D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein

[ii] HYPOTHETICAL: no

[vi] ORIGINAL SOURCES:

[A] ORGANISM: Human

[B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein
(Gc protein)

[x] PUBLICATION INFORMATION:

[A] AUTHORS: Cooke, Nancy E., David, E Vivek

[B] TITLE: Serum Vitamin D-binding Protein is a
Third Member of the Albumin and Alpha
Fetoprotein Gene Family

[C] JOURNAL: J. Clinical Investigation

[D] VOLUME: 76

[E] ISSUE: 12

[F] PAGES: 2420-2424

[G] DATE: December, 1985

[K] RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1-485

Leu Glu Arg Gly Arg Asp Tyr Glu Lys Asn Lys Val Cys Lys Glu Phe
5 10 15

Ser His Leu Gly Lys Glu Asp Phe Thr Ser Leu Ser Leu Val Leu Tyr
20 25 30

Ser Arg Lys Phe Pro Ser Gly Thr Phe Glu Gln Val Ser Gln Leu Val
35 40 45

Lys Glu Val Val Ser Leu Thr Glu Ala Cys Cys Ala Glu Gly Ala Asp
50 55 60

Pro Asp Cys Tyr Asp Thr Arg Thr Ser Ala Leu Ser Ala Lys Ser Cys
65 70 75 80

Glu Ser Asn Ser Pro Phe Pro Val His Pro Gly Thr Ala Glu Cys Cys
85 90 95

Thr Lys Glu Gly Leu Glu Arg Lys Leu Cys Met Ala Ala Leu Lys His
100 105 110

Gln Pro Gln Glu Phe Pro Thr Tyr Val Glu Pro Thr Asn Asp Glu Ile
115 120 125

Cys Glu Ala Phe Arg Lys Asp Pro Lys GLu Tyr Ala Asn Gln Phe Met
130 135 140

Trp Glu Tyr Ser Thr Asn Tyr Glu Gln Ala Pro Leu Ser Leu Leu Val
145 150 155 160

Ser Tyr Thr Lys Ser Tyr Leu Ser Met Val Gly Ser Cys Cys Thr Ser
165 170 175

Ala Ser Pro Thr Val Cys Phe Leu Lys Glu Arg Leu Gln Leu Lys His
180 185 190

Leu Ser Leu Leu Thr Thr Leu Ser Asn Arg Val Cys Ser Gln Tyr Ala
195 200 205

Ala Tyr Gly Glu Lys Lys Ser Arg Leu Ser Asn Leu Ile Lys Leu Ala
210 215 220

Gln Lys Val Pro Thr Ala Asp Leu Glu Asp Val Leu Pro Leu Ala Glu
225 230 235 240

Asp Ile Thr Asn Ile Leu Ser Lys Cys Cys Glu Ser Ala Ser Glu Asp
245 250 255

Cys Met Ala Lys Glu Leu Pro Glu His Thr Val Lys Leu Cys Asp Asn
260 265 270

Leu Ser Thr Lys Asn Ser Lys Phe Glu Asp Cys Cys Gln Glu Lys Thr
275 280 285

Ala Met Asp Val Phe Val Cys Thr Tyr Phe Met Pro Ala Ala Gln Leu
290 295 300

Pro Glu Leu Pro Asp Val Arg Leu Pro Thr Asn Lys Asp Val Cys Asp
305 310 315 320

Pro Gly Asn Thr Lys Val Met Asp Lys Tyr Thr Phe Glu Leu Ser Arg
325 330 335

Arg Thr His Leu Pro Glu Val Phe Leu Ser Lys Val Leu Glu Pro Thr
340 345 350

Leu Lys Ser Leu Gly Glu Cys Cys Asp Val Glu Asp Ser Thr Thr Cys
355 360 365

Phe Asn Ala Lys Gly Pro Leu Leu Lys Lys Glu Leu Ser Ser Phe Ile
370 375 380

Asp Lys Gly Gln Glu Leu Cys Ala Asp Tyr Ser Glu Asn Thr Phe Thr
385 390 395 400

Glu Tyr Lys Lys Lys Leu Ala Glu Arg Leu Lys Ala Lys Leu Pro Glu
405 410 415

Ala Thr Pro Thr Glu Leu Ala Lys Leu Val Asn Lys Arg Ser Asp Phe
420 425 430

Ala Ser Asn Cys Cys Ser Ile Asn Ser Pro Pro Leu Tyr Cys Asp Ser
435 440 445

Glu Ile Asp Ala Glu Leu Lys Asn Ile Leu
450 455 458

[2] INFORMATION FOR SEQ ID NO: 2:

[i] SEQUENCE CHARACTERISTICS:

- [A] LENGTH: 89 amino acids
- [B] TYPE: amino acid
- [D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein

[ii] HYPOTHETICAL: no

[vi] ORIGINAL SOURCES:

- [A] ORGANISM: Human

[B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein (Gc protein)

[x] PUBLICATION INFORMATION:

[A] AUTHORS: Cooke, Nancy E., David, E Vivek
[B] TITLE: Serum Vitamin D-binding Protein is a Third Member
of the Albumin and Alpha Fetoprotein Gene Family

- [C] JOURNAL: J. Clinical Investigation

- [D] VOLUME: 76

- [E] ISSUE: 12

- [F] PAGES: 2420-2424

- [G] DATE: December, 1985

- [K] RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 4 and 5 TO 89

Leu Glu Arg Gly Pro Leu Leu Lys Lys Glu Leu Ser Ser Phe Ile Asp
5 10 15

Lys Gly Gln Glu Leu Cys Ala Asp Tyr Ser Glu Asn Thr Phe Thr Glu
20 25 30

Tyr Lys Lys Lys Leu Ala Glu Arg Leu Lys Ala Lys Leu Pro Glu Ala
35 40 45

Thr Pro Thr Glu Leu Ala Lys Leu Val Asn Lys Arg Ser Asp Phe Ala
50 55 60

Ser Asn Cys Cys Ser Ile Asn Ser Pro Pro Leu Tyr Cys Asp Ser Glu
65 70 75 80

Ile Asp Ala Glu Leu Lys Asn Ile Leu
85 89

[3] INFORMATION FOR SEQ ID NO: 3:

[i] SEQUENCE CHARACTERISTICS:

- [A] LENGTH: 88 amino acids
- [B] TYPE: amino acid
- [D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein

[iii] HYPOTHETICAL: no

[vi] ORIGINAL SOURCES:

- [A] ORGANISM: Human

[B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein (Gc protein)

[x] PUBLICATION INFORMATION:

- [A] AUTHORS: Cooke, Nancy E., David, E Vivek
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- [C] JOURNAL: J. Clinical Investigation
- [D] VOLUME: 76
- [E] ISSUE: 12
- [F] PAGES: 2420-2424
- [G] DATE: December, 1985
- [K] RELEVANT RESIDUES IN SEQ ID NO:3: FROM 10 TO 94

Ile	Ile	Pro	Val	Glu	Glu	Glu	Asn	Pro	Pro	Leu	Leu	Lys	Lys	Glu	Leu
				5						10					15
Ser	Ser	Phe	Ile	Asp	Lys	Gly	Gln	Glu	Leu	Cys	Ala	Asp	Tyr	Ser	Glu
				20				25					30		
Asn	Thr	Phe	Thr	Glu	Tyr	Lys	Lys	Lys	Leu	Ala	Glu	Arg	Leu	Lys	Ala
				35			40					45			
Lys	Leu	Pro	Glu	Ala	Thr	Pro	Thr	Glu	Leu	Ala	Lys	Leu	Val	Asn	Lys
				50			55				60				
Arg	Ser	Asp	Phe	Ala	Ser	Asn	Cys	Cys	Ser	Ile	Asn	Ser	Pro	Pro	Leu
				65			70			75			80		
Tyr	Cys	Asp	Ser	Glu	Ile	Asp	Ala	Glu	Leu	Lys	Asn	Ile	Leu		
				85				90				94			